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1: The Amino Acid Sequence of Apo B-100

10	20	30	40	50	60	70	80	90
EEEMENLVCPKQADTRFKHLKRYVNYEAESSGVPGTADRSATRNCKKLEVEVPQLCSFLIKTSQCTLKEVYGNPEGKALLKTKNSEEFAAAMS	100							
RYELKLAIPGKQVFLYPEKOEPTYLNRKGIISALLVPETEEAKQVFLDVTYNGCSTHFTVKRGWATEISTERDLGQDRFKPIRIGTISPLAL	200							
IKGMRPLSTLISSOSQVTLDAKRKHVAETICEQLHFLPFYNNKYGMVAQVQTQLKLEDPKINSRFFEGGKTKMGLAFESTKSTSPPKAQEAIVLK	300							
TLOELKLLTISEQNIQRANL FNKL VTEL RGLSDEAVTSLPQLIEVSSPITLQALVGGGPOQSTHLQWLKR/VHANPLLIDVVTYLVALIPESQAQLR	400							
EIFNWARQDRSATLYALSHAVNNYHKTNPTGTQELLDIANYLMEQIQDDCTGDEDTYLLRVIGNWQTMEOQLPELKSSILKCVQSTKPSLMIQKAA	500							
IQALRKWEPKDQOEVLLOTLDDASPGDKRLAAYLMLRSPSQADINKITQVLPWEQNEQKNFVASHIANLINSEELDIDQLKLVKEALKESQLPTV	600							
MDFRKFSRNYOLKYSVLSPLDPAKTEGNLIFDPNMYLPKESMLKTTLTAFGASADLITETGLEGGFEPTLEALFGKQGFPPDSVNKALYVWNGQVP	700							
DGVSKVLYDHFGYTKDQHEQDMNGIMLSVEKLIKDLKSKVEPEARAYLRILGELGFASLHDLQLLGLKLLMGARTLOGIPQNMIGEVIRKSGKNDFFL	800							
HYIFMENAFELPTGAGLQLQISSSGVIAPGAKAGIKLEVAWQAEVAKPSYSVEFVTWNGIIIPDFARSGVQWNTNFHESGLEAHVALKAGLKFIIIP	900							
SPKRPVILLSSGNTLHLVSTTKTEVIPPILNQRQSWKSVQVFPGLNYCTSGAYSNWSDTSASYPLTGOTRLELELRPTGEIEQYSVSATYELQREDR	1000							
10	20	30	40	50	60	70	80	90
ALVDTLKFTQAEQAKQTEATMTFKYMRQSKTLLSSEVIQIPDFVDLGTILRWDESTGKTSYRLTLDIQNKKITTEVALMGHLSCOTKEERKIKGVISIP	1100							
RLOAEARSETLAHMSPAKLLQWSSATAYGSTVSKRYVAHYDEEKTEFEWNTGTWDTKKMTSNFPVDLSDPYKSLHMYANRLDHRVPETDMTRHVG	1200							
SKLIVAMSMWLKAGSGLPYQTLLQHLNSLKEFNLOMGLPDFHIPENLFLKSDGRVYKTLNKNLSKXIEIPLPFGGKSSROLKMLETVRTPALHFKSVG	1300							
FHLPSREFQVPTFTPKLVQLQVPLLVGLDLSTNYVSNLYNKSASVSGNNTSDHFLSARYHMKADSVDLLSYNVGSGSETTYVDHKNFTLSCDGSRLR	1400							
HKFLDSNLKFSHWEKLGNNIPVSKGLLIFDASSWGPMQASVHLDSKKKHQLFVKEVKIDGQFRVSSFYAGTYGLSCORDPNTGRLNGESNLRFNSSLV	1500							
QGTNIQITGRYEDGTLSTLSDSLQSGIKNTASLYENVELTLKSDTNGKYKNFATSKWDMTFSKQNALRSEYQADYESLRFSSLLSGSLNSHGLELN	1600							
ADLTGDKTNGSGAHKTLRIGDGTISTATNLLKCSLLVLENELMAELGSGSNKLTNGRFRHNAKFSLDGKAALTELSLGSAYQAMILGVDSKNIF	1700							
NFKVSOEGLKLNDMGSTEVAEMKFDHTNLSINLJAGSLDFSSKLDNTYSSDKFYKQTNVLQPYSLVTLTNSDLKYNALDLTNNGLRLLEPLKLHVAGNL	1800							
KGAYQNNETKHIYAISSAALSASYKADTVAKVGQVIEFSHRLNTDIAGLASADINSTVNSDSLHFSNWFRSWMAFTMTIDAHTNGKGLALNGEHTGL	1900							
YSKFLKAEPLAFTFSHDYKGTSHHLYSRKSIISAALEHKYSALLTPAQETGTWKLKTQFNWNNVYSQDLDAYNTKDKIGVELTGRTLADLTLLDSPIKVP	2000							

FIG. 1

10 20 30 40 50 60 70 80 90 2100
 LLLSEPINIDALEWRDAVEKPRQEFITVAFVYKONQDVHSINLPFFETLQEFYFERNQRTIIVVWVQORNKHINIDQFVRKRAALGKLPQANDYLN
 2200 SPMFEROVSHAKEKLTALTXYRITENDIQJALQDANINFNEKLSQJTYMTQFDQYIKOSYDQJHOLKJATIANIDEIIEKLSLDEHYIRWNLVKTH
 2300 DLHELFIENDFINKSSGSSATJWQVDTIKYQIRIQDEKQLKHHQIONIDQHLGAQKHTEAIDVRVLDQJLGTITFSERINDEHWKHFVJNLIGD
 2400 FUEWAEKINAFRAKHILIERVEYQIQVIMDKLVELTHQYKLTETIQKLSNVLQVQIKYQFEKLVGFIDQAVKGLNLSFKFITIEDVHWKFLDKMLTKL
 2500 KFSFYOHQVDEFTNDKIREVTRORLNGEIQALELPQKAEALKFLLEETKATVAVYLESJLQDKITLILINMLQEALSASLAHMKAKFRETIEDTRORMYDMD
 2600 IQDEQLRYLSLVGVYSTLVYISDMWTLAAKNLTDFAEQYISIQMAKRWKALVEQGFVPEIKTTLGTMPAFEVLSQALQAKATFQTPDFVPLTDLRIP
 2700 SVISQINFQOLKNIKIPSRFSTPEFTILNTHPISFTIDFQVEMVKIIRTIIDQMNQSELQWIPQIYRULKVIEDIPLARITILPQRLPEIAIPEFTIPTLN
 2800 HUNDFQVDPQLHPIPEQLPHISHTIEVPTFGKLYSTLKIQSPLFTLDANAQINGITTSANEAGJAASTITAGKESKLEVLNDFDQAVQALSNPKINPLALKE
 2900 VKFSKYLYRTEHGSEMFLPFGNAIEGKSNVASLHTEKNLTLSNGVYVTKWINQJLTDSNTYFHKLNIPKLODFSQADLRNEIKTLLKAGHTAVTSXGK
 3000 SHKIKIACPRFSDEGTHESQISJFTIEGRLTSFGLNSKINSKLRVQNQLVYESSGLNFSKLEIQSQVDQSQVGHVHSITAKGMALFGEKGAEFTTGRHDAHLN
 10 20 30 40 50 60 70 80 90 3100
 KGVIGTLKNSLFFSAQPEITASTNWEGNLKYRFPRLRTGKIDFLNMYALFLSPSAQQAQSNQISARFNQYKYQNQFSGAGNMENTMEAHVGINEANLDFLN
 3200 IPIPLIPITPEMLPYTIIITPPLKDFSLMEKTLKFEFLTKQSDPLSVAQKSNKRRHSITNPLAULCEFIQSITKSFDRKRNNAQDFVTKSYNETK
 3300 IKFQIKYAEKSHODELPRTFQIPQJYTPVWVNEVSPTTIEWSAFGYFPAKSNMSPFSITGSDVRWPSYTLILPSLEPLHVIPRNKLKSLPHFKLETSK
 3400 HIFITFIPAGNITVYESFKFSJITLTNMAELFVQSDIOVAHILSSSSSVFIDALQYKLEGTIRLTRKGLKATALSLSNKPFVEGSHVSTLPSHMEVSAK
 3500 TITTKAEIPLIRMNFKDELNGITKXPTVSSSMFKYQFNPSSMLYSTAKGAVOHKLSLESLTSYFSESSTKGQVGSVLSREYSGTGTASEANTYLNKSKSTR
 3600 QGTSKIDDTNMLEVKENFAGEATLQRTYSMEHSTKHNHQLLEGLFTTNGEHTSKATLELSPWQNSALVQVHASQSPSFHOFPDLQGEVALNANTK
 3700 HUNQKIRMKNEVRTHSGVSQSQSELENDQEKALHDTAGSLSEHLRFLKNLILPIYQKSLWDFLKLDDVTITSIGRRCHRLVISTAFVYTKNPNQVGSFIPYKVAL
 3800 OKFTITPGLKNDLNSNLNWMPTFHVFPFDQLQPSQKDLDFREIQYKKLRTTSFALNPLTARFEVQSPVYVAWSALSNKADYVETLDTSCSTQSVQFTL
 3900 PKYSYDQGIJALDLNVAANKIADOFELTIIIVPEQITIEPISIKFSPVAGIPIVPSQALPERFVQSPVYVAWSALSNKADYVETLDTSCSTQSVQFTL
 4000 NLNLTGIDTGLASKTGLTAHROFSAEYEEQGEKFLQEWEGKAHLNITKSPAFDHLRYQKQKIGLITSAAQPAVGTIGWMDDEDDQFSKNMFVYS

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10 20 30 40 50 60 70 80 90
 PQSSPKKL TIFKTEL RVSEDEETQ IVMNEEEAASGLTSL KQNVPKATGVL YDYVKNKYHMEHTGL TLREVSSKLRRLQNNAEWYQGAIRQIDDDID 4100
 VRFQKAASGTTGTQENKDKAQNLYQELLTQEGDASFQGLKQNVFDGLVRVTQKFHMKVKHL IDSLIDFLNFRPQFPGKPGIYTREELCTMFIREVGTV 4200
 LSQVSKVHNGSEILFSYFQDLVITLPEFLRKHLIDVISMVRELLKQLSKEAQEVFRAIQSLKTTEVLRLNQDLQFIFQLIEDNIKQLEKMFYTLIN 4300
 YIQDEINTIFNDYIPYVFKLKENLCLNLHKFNEFIQNLQEAQELQCIHQYIMALREEVDPSTVGMVTKYVELEEKIVSLIKNLLVALKDFHSEYIV 4400
 SASNFTSQLSSOVEQFHRNTOEYLSLTDPDGKGKGIKIELSATAQEIIKSQAIAATKKIISDYHQFQRYKLQDFSQQLSDYYEKFIAESKRLIDLSION 4500
 YHTFLIYITELLKKLQSTTVMNPYMKLAPGELTIL

FIG. 1 Cont.

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Comparison of SH3-like Regions in Apo B-100 to Known SH3 Domains of Signal Transduction Proteins. Percent similarities are indicated at Right margin.

	10	20	30	40	50	60	
B1	KYTNYEA--ESSSGVPGTAQSR-SATRINCKVELEVQLCSFILKTSQ						
R9	AYDFNYPKKDSSQLL-SVQQGETIYILN-KNSSGMDG--LVIDDSN						
	Y**NY * *SSS ** *** ** *N K *** *** S*						55%
B2	WGFNPEGKALLKTKNSEEFAAANSRYELKLAIPGKQV--FLYPE						
R33	LYDFVASGDNLTLSITKGEKLRVLGYNHYNGEWCEAQTNGGGWPSN						
	*Y F * G L TK ***** *Y* * ** K* *** *						51%
B3-1	FLPFSYNNKYGWAQVTQTLKLEDTPKINSRFF-GE-GTKKNGLAF						
R35	LFDYKAQREDELT--FTKSAIIQWVEKQEGGMRGDYGGKKQ-LWF						
	** * ** * *T ** *** K * ** G* G KK L*F						54%
B3-2	FLPFSYNN-KYG-MWAQVTQTLKL-EDTPKINSRFF-GEGTKKH---GLA-FE						
R18	LH--SYEPHSGDGLGFEGEQLRILEQSGE-----LWKAQ-SLTGQEGFIPFN						
	* SY* * G ***** * L** E** ** ** * G** F*						51%

FIG. 2A

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Comparison of SH3-like Regions in Apo B-100 to Known SH3 Domains of Signal Transduction Proteins. Percent similarities are indicated at Right margin.

B4	YTYLIRVINGQTMEOQLTPEL-KSSILKCVOSTKPSLMIQKAAIQALRKMEPKDKD---QEVLL	
R52	VVALFD-YAA-VNDR-DL--QVLKGE--K-LQVLRSTG--DWMLARSLVTG--REGVWPSNFVAP	
	* *L* *** * * *L ** K K *Q * * ***** *L ** **	50%
B5	AFGFASADLIEIGLEGKGFEPTLEALFGKQGFPPDS-VN--KALYVWNGQVDP	
R34	LYDFAAENPDELTFNEGAVTVINKSNP-D-WH-EGELNGQGVFPAS--YVE	
	FA* ** E* ** ** * ** * *N ** ***	59%
B8	FGYTKDKHEQ-DWVNGTMLSVEK--LIKOLKSK--EV-PEARAYLRILGEE	
R25	YDYKKEE--EDITOLHLGDIITVNGSLVALGFSQGQEAKEPTEIGWLNQY-NE	
	* Y K** E* D* G ***V*K L** S E* PE **L * *E	56%
B8	FDYHQFVDETNDK-IREVTQRLNGEIQ-ALELPQKAEALKLFEETKAT-V-AVYL	
R32	YDY-----QEKSPREVTYKK-GDILTLLNSTNK-DWVKVEVND-RGQFVPAAYV	
	*DY *** *REV* * G*I *L* *K ***K* *** * V A*Y*	52%

FIG. 2B

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B9-1	YDM--DIQELQRLSLVGQVSTLVITYISDMWT--LAAK-NLTDFAEQYSIQDWA	
R35-2	FDYKAQREDELFTTKSAITONVEKQDGG---IMRGDYGGKKQLW-FPSNY-VEEMI	
	*** * **EL S** Q * WM ***K *L F* *Y *****	54%
B9-2	YDMDIQ---QELQRLSLVGQVSTLVITYISDMWTLAANKLTDFAEQ-YSIQDWAKRMK	
R43	IQ-DYEPRLTDEI-RI-SL-GEKYK-ILATHDGNCLVEKCNTRKGTIHSVDD--KRYL	
	*Q D** *E* R* SL G* * *** *D W L* K T * *S**D KR*	57%
B9-1	YQMDI--QDELQ--RYLSLVGQVSTLVITYIS-DWM---TLAA-KNLTDFAEQYSIQDWA	
R49	YDYEARTEDDLFTTK-----GEKF-HILNNTGEDMWEARSLSSGK--T--G-CIPSNYYVA	
	Y**** **L * G* * ** DWM *L** K T * * *A	51%
B10	TYDFSFK---SS-VITLNTNAE-LFNQSDIVAHLLSSSSVIDALQY-----KLE	
R9-2	DFNYPICKDSSQLLSVQ-QGETTY-----ILNK--NSS-GWMDGLVTDSSNGKVN	
	DF ** K SS *****E ** I* * SS **D*L * K**	56%
B11	KYDFNSSMLYSTAKGAVDHKLSLESLTS-----YFSIESSTKGDVKGSVLSREY	
R47	EPYVAIK-AYTAVEGDEVSLLEGEAVEVHKLLDGMVIR---KDDVTGYFPSWYL	
	* * *Y**** G L E** ** I K DV G **S *	50%

FIG. 2C

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Comparison of SH3-like Regions in Apo B-100 to Known SH3 Domains of Signal Transduction Proteins. Percent similarities are indicated at Right margin.

B12	LUDELKLD-----VTTISGRQHLRVSTA-----FVYTKNPNGYSFSPVKVLADKFITPGLKL	
R3	LYDF-KAEKADELTTYG--ENL-FICAHHCENFIK-PIGRLLGGPGL-VPVG-FVSI-IDI	
	L*DF K** *TT *G * L * A ****K P G * * V** F*** * *	54%
B13	VLVDYVWKY-HMEHTGLT-LR-EVSSK-LRRNLQNNAEWYQGAIRQDDI	
R3-2	VLDF--KAEKADE--LTTYGENLFICAHN-----CEWFI---AKPIGRL	
	VLVD* K* *** LT * E ***N EN** ** I *	51%
B14	KPGIY--TREELCTMFIREVGTVL-----SQVYSKVHNGSE--ILF-SYFQ--DL	
R36	LFGFVPETKEELQ-VMPGNIVFVLKGNDAWATVM--F-NG-QKGLVPCNYLEPVEL	
	G* *T*EEL * ** VL * V* * NG * *** *Y** *L	56%
B15	GKPGIYTREELCTMFIREVGTVLSQ-----VYSKVHNGS-E----ILFS-YFQ--D	
R59	AKFDVAAQEQE LDIKKNERLLDDSKSM-RVRN-SMNKTGFVPSNYVERKN	
	K *** *E * I* ** ** */*N S * ***S Y** *	53%

FIG. 2D

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Identification of the regions of apo B-100 and the proteins compared in Figures 2A-2D.

<u>Reference Protein Name:</u>	<u>SEQ ID NO.</u>
Apo B-100 region B1 (aa 24-69)	SEQ ID NO:3
r9 (aa 66-114). cell division control protein 25 gim 4857	SEQ ID NO:4
Apo B-100 region B2 (aa 75-119)	SEQ ID NO:5
r33 (aa 69-114). Abl proto-oncogene tyrosine kinase (P150) gim 13887	SEQ ID NO:6
Apo B-100 region B3-1 (aa 240-283)	SEQ ID NO:7
r35 (aa 799-841). 1-Phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma (PLC-gamma. PLC-II) gim 18895	SEQ ID NO:8
Apo B-100 region B3-2 (aa 240-284)	SEQ ID NO:9
r18 (aa 69-114). Lck proto-oncogene tyrosine kinase (P56-LCK) gim 14213	SEQ ID NO:10

FIG. 2E

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IDENTIFICATION OF THE REGIONS OF APO B-100 AND THE PROTEINS
 COMPARED IN FIGURES 2A-2D

Apo B-100 region B4 (aa 457-518)	SEQ ID NO:11
r52 (aa 57-109). BLK protein tyrosine kinase (B lymphocyte kinase) (P55-BLK) giml13991.	SEQ ID NO:12
Apo B-100 region B5 (aa 652-700)	SEQ ID NO:13
r34 (aa 984-1031). Myosin IC heavy chain giml16466	SEQ ID NO:14
Apo B-100 region B6 (aa 711-756)	SEQ ID NO:15
r25 (aa 12-61). Phosphatidylinositol 3-OH giml18072	SEQ ID NO:16
Apo B-100 region B8 (aa 2403-2454)	SEQ ID NO:17
r32 (aa 976-1021). Spectrin alpha chain, brain giml23407	SEQ ID NO:18
Apo B-100 region B9-1 (aa 2497-2547)	SEQ ID NO:19
r35-2 (aa 800-850). 1-Phosphatidylinositol-4, 5-bisphosphate phosphodiesterase gamma. (PLC-gamma, PLC-II) giml18895	SEQ ID NO:20
Apo B-100 region B9-2 (aa 2497-2551)	SEQ ID NO:21
r43 (aa 444-496). Nuclear fusion protein FUS1 giml9498	SEQ ID NO:22
r49 (86-134). Fgr Proto-oncogene Tyrosine giml14097	SEQ ID NO:23
Apo B-100 region B10 (aa 3311-3355)	SEQ ID NO:24
r9-2 (aa 66-114). Cell division control protein 25 giml4857	SEQ ID NO:25
Apo B-100 region B11 (aa 3434-3482)	SEQ ID NO:26
r47 (aa 229-280). Neutrophil Cytosol Factor 1 (NCF-47K) giml16659	SEQ ID NO:27
Apo B-100 region B12 (aa 3657-3710)	SEQ ID NO:28
R3 (aa 162-201)Bem-1 protein giml3905	SEQ ID NO:29

FIG. 2F

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IDENTIFICATION OF THE REGIONS OF APO B-100 AND THE PROTEINS
COMPARED IN FIGURES 2A-2D

Apo B-100 region B13 (aa 4053-4099)	SEQ ID NO:30
r3-2 (aa 163-214)Bem-1 protein giml3905	SEQ ID NO:31
Apo B-100 region B14 (aa 4180-4222)	SEQ ID NO:32
r36 (a 248-299). Neutrophil NADPH oxidase factor (P67-PHOX) giml16660	SEQ ID NO:33
Apo B-100 region B15 (aa 4179-422)	SEQ ID NO:34
r59. Cytoplasmic protein giml16669	SEQ ID NO:35

FIG. 26

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Comparison of SH2-like Regions in Apo B-100 to Known SH2 Domains of Sign Transduction Proteins.

9.	WYHSLTRAQAEHMLMV-----PRDGA-FLVRKRNPNYSATISFR-AEGKIKH	
10.	FFEGEG-TK-----KMGAFESTKSTSPKQ-AEAVLKTLQELKKLTISEQNIQ-RANIL	
	** T* *M * * p** A **** *E* ***S **	
9.	C-RVQEGTVMIGNSEFDSLVDLISYYEKHPL-----YRKMKLK	
10.	FNKLVTQLRGLSDEAVT-SLLPQLIEYSSPITLQALVOCGQOSTHLLQWLKRVHAN	40%
	** E * * * * SL* *LI * L *****	
5.	WFHG--KISKQEAYNLLMTVGQACFLVRPS-DNTPGDY-SLVFRTSENIOQRFKICP	
11.	IMLSVEKLIQDLKSKE---VPEAR-AYLRILGEEL-G-FASLHQLQLLGLKLLMGAR	
	** K* K* V *A ***R* ** G * SL *	
5.	T-----PNNQFMGGRYYN-SSIGDITDHYRK-EQIVEGY--LKEP	
11.	TLQGIPO---MIGE-VIRKGSKNDFELHYTFEMENAFELPTGAGLQL	
	T P* MNG ** S D** HY E***E * **	42%

FIG. 3A

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Comparison of SH2-like Regions in Apo B-100 to Known SH2 Domains of Sign Transduction Proteins.

5. MFHGIS---KQEAYLLMTVQACSLVRPSDNTPGOSLYFRTSENIQ---R---F
16. YEH---KLIPK---LD---FSS---QAD---LR---NEIK---TLL---KAGHAMTSSGKGSW
FH K K ** ** QA *R ** *L* ** * *
5. KI---CPTPNOFMMGGRYNSSGIIDHYRKEQIVEGYLK
16. KWACPRFSDE---GTH---ESQISFTIEGPLTSFGLSNKINS
K* CP * ** G * *S I * * * *
6. WYWGDISR---EEWE---KLRTPDGTFLVRDASSKIQG---DYTLTLRKGGNNKL
17. FESAQPEITASTNEGNLKVR-----FPLR---LTGKIOFLNNYALFLSPSAQAS
** *** NE K*R F**R ** KI* *Y*L L ***
6. IKVFHR---DGKYG---FSEPLTFCSVDLITHRHESLAOYNAKLDTRLLYPVSKY
17. WQVSARFNOYKNQNFSAGNNEN---IMEA---HVGINGEANLD---LNIPLTIPEMRL
* V R * KY FS **E* H* * A*** L** L *P **

41%

55%

FIG. 3B

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Comparison of SH2-like Regions in Apo B-100 to Known SH2 Domains of Sign Transduction Proteins.

8.	WFHGKLGAG-RDGRHIAERLLTEYCIETGAPDGSFLVRESETFVGD-YTLSEFMRNGK	
21.	EP-GKPGITYTRE-----ELC-----TMEIREVGTVLSQVYSK--VHNGS	
	** GK*G* R* E*C ****RE T** * Y* **NG	
8.	VOHCRIHSRQDAGTPKFLLTDNL-VFD--SLY-DLITH-----YQQVPLRCNEFEFMRLE	
21.	-EILFSYF-QDLVITLPFELRKHKLIDVISMYRELL-KQLSKEAEV-FKAIQS-LKTTT	
	* QD* *F **D S*Y *L* * Q*V ** * ** *E	34%

Structurally important motifs are indicated by double underline. Percent similarity is right.

FIG. 3B Cont.

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Identification of the reference proteins as well as the apoB-100 regions used in the above alignments

<u>Reference Protein Name:</u>	<u>Sequence ID</u> <u>No.</u>
9. = phospholipase C γ 1. Residues 668-753	SEQ ID NO:36
10. = Apo B-100 region 10. aa(271-377)	SEQ ID NO:37
5. = GTPASE-activating protein (GAP) (RAS P21 PROTEIN ACTIVATOR). Residues 348-437	SEQ ID NO:38
11. = Apo B-100 region 11. aa(727-819)	SEQ ID NO:39
5. GTPASE-activating protein (GAP) (RAS P21 PROTEIN ACTIVATOR). Residues 348-435	SEQ ID NO:40
16. = Apo B-100 region 16. aa(2861-2938)	SEQ ID NO:41
6. = p85 α . Residues 326-424	SEQ ID NO:42
17. = Apo B-100 region 17. aa(3011-3110)	SEQ ID NO:43
8. = phospholipase C γ 1. Residues 550-655	SEQ ID NO:44
21. = Apo B-100 region 11. aa(4177-4267)	SEQ ID NO:45

FIG. 3C

Comparison of the Apo B-100 SH1-like Region to SH1 Kinase Domains of Known Signal Transduction Proteins.

```

*** ***** * pxy *T * * K *** PL ** * * ** ** ***** I *G
APOB QAL-TAREVDSPYVWAT-WSASLKNKADYETVL---DSTCSTVQFL---EYELNVLGTHKIEDG
SRC Q-LY-A-VWSEPIYIVTEY-WS-KG-S-LLD-FLKGET-G-K---YLRLPQL-VDMAAQ---IASG
CFYN Q-LY-A-VWSEPIYIVTEY-MN-KG-S-LLD-FLK-DGEG-RAL---KLPNL-VDMAAQ---VAAG
HCK -AWT-K---E-PIYIITEF-MA-KG-S-LLD-FLKSDE-GSQP-LPKL----IDFSAQ---IAEG
LYN -AWT-R---EPIYIITEY-MA-KG-S-LLD-FLKSDEGG-KVL-LPKL----IDFSAQ---IAEG
CK -AWT-----QEPYIITEY-MEN-G-S-LVD-FUKTPSGI-K-LTINKL---LDMAAQ---IAEG

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FIG. 4A

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COMPARISON OF THE Apo B-100 SH1-like Region to SH1 Kinase
 Domains of Known Signal Transduction Proteins.

	140	150	160	170	180	190
	*A	* **HRD*	*A**	* **	K* * GL	*E* *G A** IK *
APOB	TLA-SKTKGTLAHRDF	-SAEY---	EEDG----	KF-E-GL-----	QEW---	EGKAHLNIK-S-P-
SRC	-MAYVE-BMNYVHRDLRAANILVGE-N--	LVCKVADFLGLARLI	-EDNEYTABQG-AKFPIKWTAP			
cFYN	-MAYIE-BMNYIHRDLBSANILVG--	NG-LICKIADFLGLARLI	-EDNEYTABQG-AKFPIKWTAP			
HCK	-MAFIEQR-NYIHRDLRAANILVS---	ASLVCKIADFLGLARVI	-EDNEYTABEG-AKFPIKWTAP			
LYN	-MAYIE-RKNYIHRDLRAANVLVSE---	SLMCKIADFLGLARVI	-EDNEYTABEG-AKFPIKWTAP			
LCK	-MAFIEER-NYIHRDLRAANILVS--	D-TLSCKIADFLGLARLI	-EDNEYTABEG-AKFPIKWTAP			

	200	210	220	230	240	250	260
	A* **	** K D	GI *	** *	P *G **	** ** *	** Y P PD
APOB	AFTDLHLRYQ-K-DKK--	GI--S--	TSAA-SPAVG-TVGMDMEDDDFSKWNFYSPQSS--	PD			
SRC	AAL-Y-GRFTIKSDVWSFGILLTELTTKGRVPYPGM-VNREVLQVE--	B--GYRMP---	CPPE				
Cfyn	AAL-Y-GRFTIKSDVWSFGILLTELVTKGGRVPYPGMN-NREVLEQVE--	B--GYBMP---	C-PQ				
HCK	AI-NF-GSFTIKSDVWSFGILLMEIVTYGRIPYPGMS-NPEVIRALE--	B--GYBMPR----	PE				
LYN	AI-NF-GSFTIKSDVWSFGILLYEIVTYGKIPYPGRT-NADVMTAL--	S--QGYBMPRVENC	PD				
LCK	AI-NF-GSFTIKSDVWSFGILLTEIVTHGRIPYPGMT-NPEVIQNLE--	R--GYBMVR----	PD				

FIG. 4B

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Identification of the Apo B-100 SH1-like Region and
 the SH1 Kinase Domains of Known Signal Transduction
 Proteins and Their Corresponding Sequence
 Identification Numbers

Reference Protein	Sequence ID No.
ApoB (aa 3804-4006)	SEQ ID NO:46
SRC (aa 275-488)	SEQ ID NO:47
FYN (275-488)	SEQ ID NO:48
HCK (268-480)	SEQ ID NO:49
LYN (252-469)	SEQ ID NO:50
LCK (250-462)	SEQ ID NO:51

FIG. 4C

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The Inter-Kringle Proline-Rich Regions of Apof[a] are Compared to
 Proline-Rich Region of SH3-Binding Protein 1 (3BP1).

3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr2	-SDAEG-TAVAPPTVTPVPSLEAPSE-QA-----PTEQR-PGVQE	SEQ ID NO: 58
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr3	-SDAEG-TAVAPPTITPISLEAPSE-QA-----PTEQR-PGVQE	SEQ ID NO: 59
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr4	-SDAEW-TAFVPPNVILAPSLAEPSE-QA-----L-TEE-TPGVQD	SEQ ID NO: 60
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr5	---L-V-TE--SSVLATLTVPVDPST-EASSEEAPTAQ-SPGVQD	SEQ ID NO: 61
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr7	P--VMESTLLTTPVVPVPSLEAPSE-EA-----PTEN-STGVQD	SEQ ID NO: 62
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr8	P--VTESVLTTPVAPVPSLEAPSE-QA-----PP-E-KSPVQD	SEQ ID NO: 63
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr9	-SETE--SGVLET--PTVVP--E-PSM-EAHSEEAPTAQ-TPVVRQ	SEQ ID NO: 64
3BP1	TS-LRAPT-MPPP-LPPVPP-Q-PARRQRR--LPA---SPVIS	SEQ ID NO: 57
1kr10	-SDTESGTWAPPTV--I---QVPSL-----GPPSEQD-	SEQ ID NO: 65

FIG. 5A

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Identification of the Inter-Kringle Proline-Rich Regions
 of Apo[a] and the Proline-Rich Region of SH3-Binding
 Protein 1 (3BP1) compared in FIG. 5A.

Reference Protein	Sequence ID No.
3BP1	
Proline-Rich Region of Sh3-Binding protein 1	SEQ ID NO:57
tkr2 amino acids (106-141)	SEQ ID NO:58
tkr3 amino acids (3322-3357)	SEQ ID NO:59
tkr4 amino acids (3436-3471)	SEQ ID NO:60
tkr5 amino acids (3550-3585)	SEQ ID NO:61
tkr7 amino acids (3770-3805)	SEQ ID NO:62
tkr8 amino acids (3884-3919)	SEQ ID NO:63
tkr9 amino acids (3998-4033)	SEQ ID NO:64
tkr10 amino acids (4112-4137)	SEQ ID NO:65

FIG. 5B

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Proteins Are Compared to the Analogous Regions in Apo B-100.

	*K*A***	R*	****	**	**G*	G***	* *	***	
B100(13-49)	PKD	ATRFKHLRKY	TYN	YEA	ESSGV--	PGTAD--	SRS	ATRI	(SEQ ID NO:66)
SRC(7-40)	PKD	AS----	QRR	SLEP-	AENVHGA-	GGGA	FPAS	QTPSKP	(SEQ ID NO:67)
FYN(7-38)	DKE	ATKLTE	ERD	GS	LN----	Q-SSG	YRYGT-DP----	TPQHY	(SEQ ID NO:68)

FIG. 6A

	***	*	TF	Y*	*L	*	**T	*P	Y	PGE	L	
apoB-100 (4448-4536)	IQNVH-	TF	LIYIT	ELL	KKL	QST	TV	MNP-	YMK	LAP	GE-L	TTIL (SEQ ID NO:69)
SRC(505-535)	PEE-	RPTF-	EY	LQAF	LED	YFT	ST--	EPQ	YQ---	PGE	NL----	(SEQ ID NO:70)
FYN(506-536)	PEE-	RPTF-	EY	LQSF	LED	YFT	AT--	EPQ	YQ---	PGE	NL----	(SEQ ID NO:71)
HCK(498-526)	PEE-	RPTF-	EY	IQSV	LDD	FYT	AT--	ESQ	YQQQ-P-	-----		(SEQ ID NO:72)
LYN(483-511)	AEE-	RPTF-	DY	LQSV	LDD	FYT	AT--	EGQ	YQQQ-P-	-----		(SEQ ID NO:73)
LCK(480-508)	PED-	RPTF-	DY	LRSV	LED	FYT	AT--	EGQ	YQPQ-P-	-----		(SEQ ID NO:74)

*indicates conserved amino acids

FIG. 6B

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Examples of Proline Pipe Helix Structures in ApoB-100

SEQ ID NO:	Sequence	Sequence Source
77	PQNAKLKIRPVKVQPIARWY	Tus proline pipe (223-243)
78	PDFRLPEIAIPEFTIPTLNLD	ApoB-100 (2682-2702)
79	NDFQVPDLHIPEFQLPHISHTI	ApoB-100 (2702-2723)
80	PSLELPVLHVPRNLKLSLPHFK	ApoB-100 (3273-3294)

FIG. 7

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Sequence Comparison of DNA-Binding Protein ISGF3 γ SEQ ID NO:81, and a Similar Region of Apo B-100 SEQ ID NO:82, Located Between Residues 0008 and 0393.	
LDLRLVAEPGSESS-ME-QVLF-PKPGPEPTQRLLSQLERGIIVASN KEQHLFLPFSYKNKYGWVAQVTQTLKL--EDTPKINSRFFGEGTKKMG * <u>KL</u> ** *S* M QV * <u>K</u> * E T ** S*	ISGF3 γ apoB100
PRGLFVQ--RLCPTISWNAQAPPQPGPHLLPSNECVELFRTAYFCR ---LAFESTKSTSPPKQAEAVLKTQLKRLTISEQNIQ--RANLFNK L*** * <u>W</u> * *p- *A* - * * <u>L</u> * S** ** R* *F *	ISGF3 γ apoB100
DLVRYFQGLGPPPKFQVTLNFWEEHSGSSHTPQNLITVKMEQAFARYL -LVTELRLGSDAEVTSLLPQLIEVSSPIT-LQALVCCGQPCSTHTL LV * <u>GL</u> * * ****E S * *Q L* Q ***L	ISGF3 γ apoB100
KMEQAFARYLLEQ-TPEQQAAILSLV KRVHAMP-LLIDVVTY---LVALIPE <u>K</u> A * L** T* ***L *	ISGF3 γ apoB100

* Indicates conserved amino acids
 bold type indicates positively charged, basic amino acids

FIG. 8A Cont.

Sequence Comparison of DNA-Binding Protein ISGF3 γ , SEQ ID NO:81, and a Similar Region of Apo B-100 Located Between Residues 2930 and 3324, SEQ ID NO:83.

FIG. 8B

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Sequence Comparison of DNA-Binding Protein ISGF3 γ SEQ ID NO:81, and a Similar Region of Apo B-100 Located Between Residues 2930 and 3324, SEQ ID NO:83.

IYGRVGEAQVQLDRLVAEPSSGESSMEQVLFPKPGPEPTORLL ISGF3 γ
 HRHSTINPLAVLCEFIQSISKSFDRHFKEKRNNALDFVTKSYNETKIK apoB100
 * * * * * E * * * * *

SQLERGILVASN-PRGLFVORLCIPISWNAPOAPPGGPHLLPSNE ISGF3 γ
 FDKYKAEKSHDELPRF-FQIPGYTPV-VNVEVSPFTIEMSAFGYVF apoB100
 * * * * * PR FV * p * * * * *

CVLELFRITAYF---CRDLVRVYFQGLGPPPKFQVTLNFWEEESHGSSHTP ISGF3 γ
 -PKAVSMPSFSLGSD-VRVPSYTLILPSLELPVLHVPRNEKLSLPH apoB100
 * * * * * F D VR** **p *** * * * * S

-QNLITVKMEQAFARYLLEQTPEQQAAILSLV ISGF3 γ
 FKELCTISHIFIPAMGNITYDFSFKSSVITLN apoB100
 &L T * * * * * * * * * * *

* Indicates conserved amino acids
 bold type indicates positively charged, basic amino acids
 ISGF3 γ = sequence ID No:81, Apo B-100 amino acids (aa 2930-3324) = sequence ID NO:83.

FIG. 88 Cont.

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Various regions of apoB-100 having similarity of ISGF3 γ (1-51)

SEQ ID NO:	
84	ISGF3 γ (1-51)
85	APOB(13-59)
86	APOB(80-116)
87	APOB(159-196)
88	APOB(363-413)
89	APOB(1082-1119)
90	APOB(1441-1487)
91	APOB(2073-2113)
92	APOB(2114-2153)
93	APOB(2281-2330)
94	APOB(2390-2439)
95	APOB(2933-2955)
96	APOB(2956-3001)

MASGRARCTRLRNWVEQVESGQPGVCHDDTAKTFRIPMKHAGKQDFR
 --PKDATRFKHLRKYYTNVEAESSGVPGTAD--SRSATRINCKVELEVLPQ
 --PEGKALLKTKINSEFAAM-----SRVELKLAIP-EGKQVFL
 --CSTHTVTKTRKGNWATEIST-----ERDLGQCDRFKPIRTGIS
 CSTHTLQMLKRVYHANPLLIDVVTYVALIPEPSAQLREIFNWARDQSRRA
 HLCSDTKERKTKGVISI-----PRLQAEARSEILAHNSPAKL
 --SVHLDSKKQHFLFVKEVKIDGQFRVSSFY--AKGTYGLSCORDPNTGRLL
 KHINIDQFVRKYRAALGKLPQANDYLSFNWERQVSHAKE-----
 ---KL TAL TKYRITENDIQIA-----LDDAKINFNEKLSQLQTYMIQ
 -ERINDVLEHVHKVFVINLIGDFEVAEKINAFRAKYVHELIEREYVDQIQVL
 -NKFLDMLTKKLKSFQYHQFVDETNDKIREVTORLNGETQALELPQKAEAL
 ----SNKINSKHLRVNQNLVYESGSLN-----
 ----FSKLEIQSQVDSQHVGHSL TAKGMALFEGGKAEFTGRHDAHLNGK

FIG. 9A

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Various regions of apoB-100 having similarity of ISGF3 γ (42-69)

SEQ ID NO:		
104	iSGF3 γ (42-69)	KAWAIFKGYKEG-DKEVPERGRMDVAEPYK
105	APOB (2288-2335)	FEVAEKINA-FRAKVHELIERYVDQQIQVLMQKLV
106	APOB (2081-2132)	VRKYRAALGKLPQANDYLNFSNFWERQVS--HAKKELTALTKYRITENDIQIA
107	APOB (2157-2213)	YIKDSYDLHQLKATATANIIDEIIEKIKSLDEHYHIRVNLVKTTIDHLHLFIENIDFNK
108	APOB (2461-2493)	-----KITLIINWLOEALSSASLAHMKAKFRETLIEDTR-----
109	APOB (1353-1385)	-----TDHFSLRARYHMKADSWDLSYNVQSGSETTY-----
110	APOB (1656-1675)	-----KLTTNGRFRFHNNAKFSLOGK-----
111	APOB (2226-2277)	DTKYQIRIQIQEKQLQKRHIQNIQIHLQAGKIKQHIEAIDVRVLDQLGTT-----
112	APOB (3583-3627)	-----FHDFPOLGQEVAVANTKNOKIRMKNEVRTHSGSFQSQVELSNDQ-----
113	APOB (4141-4174)	-----KQWFDGLVRVTKQFHMKVKVHLIDSLIDFLNFR-----
114	APOB (4418-4452)	-----HRNIQEVLSILTPDQGGKEKIAELSATQETIKS-----

FIG. 9B

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Sequence Comparison of DNA-Binding Domains of SREBP 1 (aa 279-452) SEQ ID NO:116, SREBP 2 (aa 287-568) SEQ ID NO:117 and ADD1 (aa 250-421) SEQ ID NO:118 to a Similar Region of Apo B-100 (aa 2024-2234) SEQ ID NO:115.

EFTIVAFKYDNQDVHSINLPFFETLQEFERNQRTIIVLENWQ	APOB100
GPLPTLVSGGTILATVPLVDAEKLPIINRLAAGSKAPASQSR-GE	SREBP1
QVPTLVGSSGTILTTNPVMMGQEKVPICKQVPGGVQK-LEPPKE-GE	SREBP2
GPLQTLVSGGTILATVPLVVDTKLPIHRLAAGGKALGSAQSR-GE	ADD1
***** V * * * ***** *Q * * * E *	
RKLKHINIDOFVRKYRAAL-GKLPOQANDYLSNFWERQVSHAKEK	APOB100
KRTAH-NAIE--KRYRSSINDKIIEIK-DLVVGTEAKLNKSAVERK	SREBP1
RRTH-NIE--KRYRSSINDKIIEIK-DLVVGTDAMHKSGLVRK	SREBP2
KRTAH-NAIE--KRYRSSINDKIVELK-DLVVGTEAKLNKSAVERK	ADD1
R* H NI * **YR*** K*** D** * * S * K	
LTALTKKYRITEND-IQIALDDAKINFNEKLS-----QLQTYNIQF	APOB100
AIDYIR-FLOHSNQKLKQENLSLRITAV-HKSKSLK--DLVSAC---	SREBP1
AIDYIK-YLQQVNHKLKQENMWLKLAK-NQKNKLLKGDIGSLV---	SREBP2
AIDYIR-FLOHSNQKLKQENLTIRSA--HKSKSLK--DLVSAC---	ADD1
* * K Y N* * *K* *N*K *L ***	

FIG. 10A

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Sequence Comparison of DNA-Binding Domains of SREBP 1 (aa 279-452)
 SEQ ID NO.: 116, SREBP 2 (aa 287-568) SEQ ID NO.: 117 and ADD1 (aa
 250-421) SEQ ID NO. 118 to a Similar Region of Apo B-100 (aa 2024-2234)
 SEQ ID NO.: 115.

DQYIKDSYDLHD-LKIAIANIIDEIIEKLKSLDEHYHIRVILVKTI	APOB100
GSGG-NTDVLMEGVK-----	SREBP1
DN-----EV-D-LKI-----	SREBP2
GSGGG-TDVSMEGMKP-----	ADD1
D* ** ** D LKI	

HDLHLFIENIDFN-----KSGSSTASWIGNVDTKYQIRIQ	APOB100
-----TEVEDTL--TPPP-SDAGSPFQSSPLSLGSRGSGSGG	SREBP1
-----E-DFNQNVLLMSPPASDSGSQAGFSPYSIDSEPGSPLL	SREBP2
-----EVVETL--TPPP-SDAGSPSQSSPLSLGSRGSSSGG	ADD1
* DFN	SGS *** *D* * *

FIG. 10A Continued

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Sequence Comparison of SREBP1 to Apolipoprotein apo A1
 apoA1 (1-243) SEQ ID NO: 119 and SREBP1 (aa 233-500) SEQ ID NO:120

DEPQSPMDRVKDLATVYVDVLKDSGRDVYSQFEGSALGKQLNLKLDNMDSVTSTFSKLRQLGPGVTOEFWDN	apoA1
QQVPVLLQPHFTKADSLLLTAMKTDGATVK-----AAGLSPLVSGTTVQTG-PLPTLVSGG--TILATVPLWD-	SREBP
p * ** * * * **K\G ** **L * ** * * * S * */ **D	
LEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELOEGARQKLHELQ-EKLSPLGEE	apoA1
AEKLPINRLAAGSKAPASATSRG-----EKRTAHNAIEKRYRSSINDKIIELKDLVGTGTEAKLNKSAVL---	SREBP
*EK \ SK * * ** *K* */ R * * ** E* *K ***	
MRDRAR--AHVDALRTHLAPYSDELQRRLAARLEA-LKEN-----GGARLAEY-HAKATE-----	apoA1
-R-KATDYTRF-LOHSNQKLKOEENLSRTAVRKSLSKLDLVACSGSGGNTDVLMEGVK-TEVEDTLTPPPSDAG	SREBP
R**A *** * ** * *L R *** LK*	
-----HLSTLSEKAKPALEDLROGLLPVLESFKVSFLSALEEYTK--	apoA1
SPFQSSPLSLGSRGSGGSGSDSEPDSPVF-----EDSKAP--EQ-RPSLHSGRMIDR-SRL-ALCTLVFLC-	SREBP
\KAKP E* R L * S L AL *	
LNTQ	apoA1
LSCN	SREBP
L *	

FIG. 10B

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Sequence Comparison of apoAII (1-77) SEQ ID NO:121 and SREBP1 (aa 353-423)
 SEQ ID NO:122

OAKEPCVESLVSYFQVTVDYGGKLM---EKVKSPELQAEAKSYFEKSKQLTPLIKKAGTELVNFLSYFVEL-
 EARLWK--SAVLRKAI----DYIRFLOHSNQKLKQENLSL--RTAVHRSKS-LKOLVSA~~C~~CGSG-GNTD-VLMGV
 *AR\ / S*V DY * L *K*K *L L **** KSK L L* G* N ***E

apoA-II
 SREBP1

GTQPATQ
 KTEVEDT
 T** \

apoA-II
 SREBP1

FIG. 10C

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Sequence Comparison of apoAIV (30-376) SEQ ID NO:123 and SREBP1 (aa 330-1146) SEQ NO:124

QKSEL	TOQLNAL	FQDKL	GEVNTYAGD	LOKKLVF	FATEL	HERLAKD	SEKLKEE	IGKELE---	ELRA-R-LLPH	apoAIV
EKLPI	-NRLAAGS-	KAPASQ	SRGE--	KRTAH	NAIEK	RRYSSTN	-DKITE-L-	KDLVVGTEAKLNKSAVLR	SREBP1	
*R	* * * L A	K*	G* K*	* * A	E * R	* * * K*	E * R	* * * * *		
-ANEV	SQKIGDNL	RELOOR	LEPYADOL	RTQVNTQ	AEQLRR	QLDPLAQ--	RMERVL	RENADS-LQASLRPH--	apoAIV	
KADY-	TRFLQHS---	NOKL	KOENLS	LRTAVH	KS_KS-	LK-DLV	SAGSGG	NTDVLMEGVKTEVEDTLTPPPR	SREBP1	
A **	* * *	*Q	L	R T V	L * *	L * *	E * *	* * * * *		
-----	-----	-----	-----	-----	-----	-----	-----	-----		
DAGSP	FQSSPLSL	GRSGSG	SGSDSE	PDSPV	EDSKAK	PEQRP-	SLHSR----	GMLDRSLALCTLVFLC	apoAIV	
					**	KAK**Q*	L * R	* * * * *	SREBP1	
RSLAP	YADDTQ	EKLNHQ	EGLTFQ	MKKNAEEL	KARISAE	ID-QTVEEL	RRSLAP	YAQDTQEKLNHOLEGL	apoAIV	
ESCNPL	ASLLGARGL	PSPD	TTSVYH	SPGRNV	LGTESR	DGPGMAQ	AVQLF	ECDLLLVVRTSLWQQ-QPPAP	SREBP1	
S P	A	*	T	**	* * *	* S	Q*/	* * L * * * * *		
TFQMK	NAEELKARISAE	ELR--QR----	LAP	AE	DVRGNL	KGNT--	EGLQKSLAE	LGGHLDQQVEE--F	apoAIV	
APAAQ	GASSRP----	QASALE	IRGFQ	RDLSRL	RAOSFR	PAMRRVFL	HEATARL	MAGASPTRTHQLDRLS	SREBP1	
**	* *	ASA	ELR	QR	L	LA*	R * *	E * *		
RRRVE	PGENFKAL	VOOMEOL	ROKL	GPHAGD	VEGHL	S-FLEK	D-----	LROKVNSFFTFKEKESQ-DKTL	apoAIV	
RRRAG	PGGKG--	AVAE-LE-	PRPT	RR	REIA-EALL	ASCYLP	PGFL	SAPQQRVGMIAEAARTTEKLGDRRL-	SREBP1	
RRR*	P G	A ***	*E	*R	HA **	*S	*L	* * * * *		
								E * *		
								D * L		

FIG. 10D

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Sequence Comparison of apoAIV (30-376) SEQ ID NO:123 and SREBP1 (aa 330-1146)
 SEQ ID NO:124

LPELEQQQQQQQQEQVQMLAPLES
 LHDCQQ-----MLRLGGGTTVTSS
 L* *Q ** S

apoA
 SREBI

FIG. 10D Cont.

Sequence Comparison of acat (fragment 1) SEQ ID NO:125 and SREBP1
 (aa 300-486) SEQ ID NO:126

EKMSLRNRLS-KSRENPEEDED-QRNPAKESILETPSNGRIDIKQLIA
 EKLPITNRLAAGSKAPASQSRGERTAFNAIE-----
 EK* * NRL* S* * * A***E

acat
 SREBP1

KKIKLTANGRI-DIKQLIAKK-IKLTAEINGRIDIKQLIAKKIKLTAE
 KRYRSSINDKRIEIKQLVWGTEAKLNKSYIRFLOHS--NQLKQENL
 K*** **N *I **R*L** *KL R*/# R*R

acat
 SREBP1

AELKPFMFMEVGSHFDDFVT-----NLJ-EKSAS-LDNKAHSF
 S--LRTAVHKSKSLK--DLVSACSGSGNTDVLMEGVKTEVEDKARPE
 * L***R -# D*/# ***E * ***R#

acat
 SREBP1

VRENV-PR-VLNSAKEK
 QRPSTHSGMLD--RSP
 -R # R *L* # *

acat
 SREBP1

FIG. 10E

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Sequence Comparison of acat (fragment 2) SEQ ID NO:127 with
 SREBP1 (aa 1061-1085) SEQ ID NO:128

RRHC-PLKNPTFLDYVRRSMTCRYVF
 RRRAGPGGKGGAELPRPTRRH
 RR* P ** * PR
 acat
 SREBP1

FIG. 10F

Sequence Comparison of apoE (aa 124-181) SEQ ID NO:129 and SREBP1 (aa 302-
 360) SEQ ID NO:130

AMLQSTEE-LRVRLA--SHL-RKLKRLLROADDLQKRL-AVYQAGAREGAERGLSAIRE-RL apoE
 KLPINRLAAGSKAPASQSGEKRT-----AHNA--IEKRYRSSIN--DKIIEKDLVWGTEAKL SREBP1
 ** * ** ** S* ** **** **KR* * ** * \/* L * E *L
 --GPLVEQGRVRAATVGSILAGQPLQERAQANGERLARMEEGMSRT-RDRLDEVKEQVA apoE
 NKSAVL---R-KAIDYIRFLOHSNQKICKQENLS-LRTAVHK--SKSLKD-LVSAQSGG SREBP1
 *** R KA* * ** Q Q LR* S** D I * *

FIG. 10G

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Sequence Comparison of apoC-II (aa 1-42) SEQ ID NO:131 with
 SREBP1 (aa 231-275) SEQ ID NO:132

TOQPQDEMPSTFLTQVK-----ES--LSSVWE---SAKTAQNLVEKTYL	apoC-II
SQ-IQQ-----VPVLLQPHFIKADSLLLTAMKTDGATVKAAGLSPLVSGTT	SREBP1
*Q *QQ * *L Q** *S L*** **K*A* **	

FIG. 10H

Sequence Comparison of apoC-III (aa 7-51) SEQ ID NO:133 with
 SREBP1 (aa 314-360) SEQ ID NO:134

SLLSFMQGYMKHATKTAKDAL--SSVQESQVAQARGWTDGFSSLK--	apoC-I
APASAQSRGKRTAHNATEKRYRSSIND-KIIE-LKDLVVGTEAKLNKS	SREBP1
S KA *SS*** *** ** *L	

FIG. 10I

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Sequence Comparison of apo C-III (aa 52-79) SEQ ID NO:135 with
 SREBP1 (aa 717-748) SEQ ID NO:136

DYWT--VKDKFSEFWLDPEVRP--TSAVAA
 EIWAALRVKTSILPRALHFLTRFFLSARQA
 *** * ** K S * L * R * *SA A
 apoC-III
 SREBP1

FIG. 10J

Sequence Comparison of apo D (aa 30-34) SEQ ID NO:137 with SREBP1
 (aa 301-305) SEQ ID NO:138

EKIPT
 EKLPI
 EK*P
 apoD
 SREBP1

FIG. 10K

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Sequence Comparison of apo D (aa 36-65) SEQ ID NO:139 with SREBP1
(aa 361-391) SEQ ID NO:140

ENGRCIQANYS-LME-NGKIKVLNQELRADG
AVLRKA-IDYIRFLQHSNQKIKQENLSIRTAV

apoD
SREBP1

FIG. 10L

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Comparison of the Primary Structures of Known Coiled-Coil Regions of
 DNA-Binding Proteins and Analogous Regions in Apo B-100

MKQL <u>EDKVEELL</u> SKNYHLENEVARLKKLVGER	GCN4-p1	(SEQ ID NO:141)
KHEIQEMFDQLRAKEKELRTWEEELTRAALQQ	hMLK1(286-317)	(SEQ ID NO:142)
EELLRRREQELAEEREIDILEREINIIHQLCQ	hMLK1(321-352)	(SEQ ID NO:143)
RIQIQEKLQQLKRHIQIDIQHLA G KLKHIE	apoB(2232-2264)	(SEQ ID NO:144)
VLOQVKIKDYEEKLVGFIIDAVKKLNELSFKTFFIE	apoB(2353-2387)	(SEQ ID NO:145)
ELSEKTFIEDVYKFLDMLIKKLSFDYHQFV	apoB(2379-2409)	(SEQ ID NO:146)
HQFVDETNDKIREVTQRLNGEIQALELP	apoB(2406-2433)	(SEQ ID NO:147)
AAK N LTDFAEQYSIQDWAKRMKALVEQGFTV	apoB(2530-2560)	(SEQ ID NO:148)
SASLAHMKAKERETLEDTRDRMYDMDIQELQRYL	apoB(2475-2509)	(SEQ ID NO:149)
CLN L HKFNEFIQNELQEA S QELQQIHQYIMALREE	apoB(4326-4360)	(SEQ ID NO:150)
FLIYITELLKKLQSTTVMNPMKLAPGELTIIL	apoB(4504-4536)	(SEQ ID NO:151)

FIG. 11

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Comparison of Known ATP-Binding Loop Motifs to Similar Regions in Apo B-100. The critical amino acid H is indicated by (#)

A: THE HIGH LOOP		
RLLDHRVPETDMTFRHVGSKLIVAMSSWLQ	apoB(1183-1212)	(SEQ ID NO:152)
LNFSKLEIQSQVDSQHVGHSVLTAKGMALF	apoB(2954-2983)	(SEQ ID NO:153)
NQNFSAQNNENIMEAHVGVINGEANLDFLNI	apoB(3072-3101)	(SEQ ID NO:154)
MVVTRIAPSPT-GDPHVGTAYIALFNYAWA	TTETS(1-29)	(SEQ ID NO:155)
TTVHTRPPEPNGLYHIGHAKSICLNFGLA	ECQTS(25-54)	(SEQ ID NO:156)
KIKLYCGVDPTAQSLHGLNLPVWVLLHFYV	YSCMSY1(85-114)	(SEQ ID NO:157)
PIALYCGFDPTADSLHGLVPLLCCKRGQ	ECOTYRS(33-62)	(SEQ ID NO:158)
RVTLYCGFDPTADSLHIGNLAAILTLRRFQ	BACTYRSA(30-59)	(SEQ ID NO:159)
RIGAYVGIDPTAPSLHVGHLLPLMPLFMY	NEUTYRSM(95-124)	(SEQ ID NO:160)
PIALYCGFDPTADSLHGLVPLLCCKRFQ	SYE ECOLI(31-61)	(SEQ ID NO:161)
PLKVKLGADPTAPDTHLGHVTLVNLKLRQFQ	HEAHI1610(31-60)	(SEQ ID NO:162)

#

FIG. 12A

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Comparison of Known ATP-Binding loop Motifs to Similar Regions in Apo B-100. The critical amino acid K is indicated by (#)

B: THE KWSK LOOP

VSKGLIFDASSMGQMSASVHLDSKKKQHLFVKEVKIDGQF	apoB(1421-1463)	SEQ ID NO. 163
TTITPPLKDFSLWEKTLKEFLKTTKQSFDSLVAQYKKNKH	apoB(3113-3155)	SEQ ID NO. 164
KNRNVALDFVTKSYWETK----IKFDKYKAESQDELPRTFQI	apoB(3183-3221)	SEQ ID NO. 165
DALQYKLEGTTRL---TR----KRGLKLATALSLSNKFEVGGSH	apoB(3348-3390)	SEQ ID NO. 166
RAFGMEAPREYHNPILLRNPDK-TKISKRSHTSLDWYKAEGFL	ttets(221-262)	SEQ ID NO. 167
DNITIPVHPRQVEFSRLNLEY-TWMSKRKLNLLVTDKHVEGWD	ecqts(245-287)	SEQ ID NO. 168
KIKGL--PFGITVPLLTATGE-KFGKSAGNAVFIDPSINTAY	YSCMSY1(282-320)	SEQ ID NO. 169
RLHQNQ-VFGLTVPLITKADG-TKFGKTEGGAWLDPKKTSPY	ECOTYRS(215-254)	SEQ ID NO. 170
KTKGEARAFGLTIPLVTKADG-TKFGKTESGTTIWDKEKTSY	BACTYRSA(210-249)	SEQ ID NO. 171
KTALDE-CVGFTVPLLTDSSG-AKFGKSAGNAIWLDPYQTSVF	NEUTYRSM(303-343)	SEQ ID NO. 172
RLHQNQ-VFGLTVPLITKADG-TKFGKTEGGAWLDPKKTSPY	SVY ECOLI(213-253)	SEQ ID NO. 173
SAGKK-PQVAITLPLLVLGDEKMSKSLGNVIGYTEAPSDMF	HEAHI1610(202-243)	SEQ ID NO. 174

#

FIG. 12B

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A COMPARISON OF THE ATP-BINDING SITE WITH GLYCINE LOOP WHICH IS PRESENT IN SRC AND OTHER
 SINGAL TRANSDUCTION PROTEIN SH1 KINASE DOMAINS WITH THE ANALOGOUS SEQUENCE IN THE APO B-100
 SH1 REGION.

RVSTA-F--VY--TKNPNGYSFIPVKYLADKFITPGLKL APOB (3676-3710) SEQ. ID NO. 176

KLGGGCFGGEVWNGTH--NGT-----TRVAI-KTLKPG SRC SEQ ID. NO. 176

K***G*** NG VA K *

#

FIG. 12B Cont.

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Examples of Nuclear Localization Signal Sequences in the ApoB-100
 Amino Acid Sequence Compared to Known NLS Sequences.

Human apoB-100 sequences with 10 amino acids in the spacer region
 between the bipartite NLS element

SEQ ID NO.	Sequence	Source of Sequence
178	HKNTSTLSCDGLRHKF	human apoB-100 (1387-1403)
179	RKLKHINIDQFVRKYRA	human apoB-100 (2070-2086)
180	RHIQNIDIQHLAQLKQH	human apoB-100 (2244-2261)
181	KKGFYKKQCRPSKGRK	human IGFBP-3
182	KKPLDGEVFTLQIRGRER	human p53 fragment 1
183	KRALPNNTSSSPQPKK	human p53 fragment 2
184	KKTNLFSAIKKKKTA	human Ab1
185	RKTLNLSLEAKKKKED	human apoJ fragment 1
186	RRELDLSQVAERLTK	human apoJ fragment 2

FIG. 13A

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Human apoB-100 sequences with 10 amino acids in the spacer region
 between the bipartite NLS element

SEQ ID NO.	Sequence	Source of Sequence
187	RRSYALVLSLFRKLRL	human ir fragment 1
188	RRYGDEELHLCVSRKHF	human ir fragment 2
189	KRVAKRKLIEQNRERR	human thyroid receptor fragment 1
190	HRSTNAQGSIMKQRRKF	human thyroid receptor fragment 2
191	KRPPISESELSAKKRK	human af9
192	KGKKPKTEKEDVKHI	human irf2
193	RKRMNRITAAKCRKRK	human ap1
IGFBP-3 = interferon growth factor binding protein 3; apof = apolipoprotein; ir-insulin receptor; af9-activation factor 9; irf-insulin response factor 2; ap1 = activation protein 1		

FIG. 13A Cont.

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Human apoB-100 sequences with more or less than 10 amino acids
 in the spacer region between the bipartite NLS element

SEQ ID NO.	Sequence	Source of Sequence
194	RHIQNIDIQLAGLKQH	human apoB-100 (2244-2261)
195	KKITEVALMGHLSCDTKEERK	human apoB-100 (1072-1094)
196	KHINIDQFVRKYRA	human apoB-100 (2073-2086)
197	HRNIQEYLSILTDPPGKGKEK	human apoB-100 (4418-4438)

FIG. 13B

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Human apoB-100 sequences with more or less than 10 amino acids in the spacer region between an imperfect bipartite NLS element

SEQ ID NO.	Sequence	Source of Sequence
198	KEVGFNPEGKALLKTK	human APOB100 73-90
199	KVLVDHFGYTKDDKHEDM	human APOB100 705-723
200	KAGKLFIIPSPKRPVKL	human APOB100 891-908
201	RQVSHAKEKLTALTCKYR	human APOB100 2106-2123
202	KYQIRIQIQEKLQQLKRH	human APOB100 2228-2245
203	KGMALFGECKAEFTGRHDAH	human APOB100 2978-2997
204	KQSFDSLVAQYKKNKHKR	human APOB100 3139-3156
205	KLEGTTLRLTRKGLK	human APOB100 3353-3367
206	KLDVTTSGRRQHLR	human APOB100 3662-3676
207	KLDFREIQIYKKLR	human APOB100 3735-3748

FIG. 13C

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Human apoB-100 sequences with more or less than 10 amino acids in the spacer region between an imperfect bipartite NLS element

SEQ ID NO.	Sequence	Source of Sequence
208	KSPATDLHLRYQDKK	human APOB100 3952-3968
209	KYHWEHTGLTREVSSKLRR	human APOB100 4060-4079
210	KDNVFDGLVRVTQKFHMKVKH	human APOB100 4141-4161

FIG. 13C Cont.

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ALIGNMENT OF HUMAN 2041-2220 SEQ ID NO:211 WITH PIG SEQ ID NO:212 AND RAT
 SEQ ID NO:213 APOB-100 SEQUENCES

SINLPFFETLQEFERNQTTIIVVLENVORVKLKHINIDOFVRYBAALGKLPQANDYLN	Human (2041-2100)
PPQGVNDYLN	Pig (fragment 1)
KYRVALSRLPQSTHDYLN	Rat (fragment 1)
SFWWERQVSHAKEKL TALT KKYRITENDIQIALDDAKINFNEKLSQLQTYMIQFDQYIKD	Human (2101-2160)
TFSWERQVLSAKKKHDFMEDYRITENDVRIALDNAKINLNEKL TQLQTYVIQFDQYIKD	Pig (fragment 1)
ASDWERQVAGAKEKL TSPMENYRITDNDVLIALDSAKINLNEKLSQLETYAIGFDQYIRD	Rat (fragment 1)
SYDLHDLKIAIANIIDEIIEKLSDEHYHIBVILVKTIEDLHLFIENIDFNKSGSSTAS	Human (2161-2220)
NYDLHDFKTAIABIIDEIITLTKIL	Pig (fragment 1)
NYDAODL	Rat (fragment 1)

FIG. 14A

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ALIGNMENT OF HUMAN 2701-3540 SEQ ID NO:214 WITH HAMSTER SEQ ID NO:215 AND MOUSE SEQ. ID
 NO:216 APOB-100 SEQUENCES

LNDQVQDHIPEQLPHISHTIEVPTFGKLYSILKIQSPFLTLDANADIGNGTTSANEAE- Human (2701-2760)
 EFQLPRLSHTEIIPAFGRUHGILKIQSPFLTLDANANIQNVTTLENKAE Hamster (frag 1)
 EFQLPRLSHTEIIPAFGRUHGILKIQSPFLTLDANANIQNVTTSGNKAE Mouse (frag 1)
 GIAASTAKGESKLEVLNFDQANQALSNPKINPLALKESVFSSKYLRTEHGSEMLFFG Human (2761-2820)
 IVASIAAT-GESETEALNFDQAAQFLELNPPLILKESWFSKXARMHEGEILFSG Hamster (frag 1)
 IVAS-VTAKGESQFEALNFDQAAQFLELNPFPVLKESWFSKXVRMEHEGEIVFDG Mouse (frag 1)
 NAIEGKSNIVASLHTEKNTLELSNGVTVKINNQLTLDSTNTKYFHKLNPXKLDFFSSQADLR Human (2821-2880)
 KFTIEGLDVTASLQTEKINWVEFNMGMTVKINNPIILDSHTKYFHKLSTPRLDFFSSKASFN Hamster (frag 1)
 KATIEGKSDTVASLHTEKNEVEFNMGMTVKYNNQLTLDSTHTKYFHKLSTPRLDFFSSKASLN Mouse (frag 1)
 NEIKTLKAGHIAWTSQKGSIMKACPRFSDGETHESQISFTIEGPLTSFGLSNKINSKH Human (2881-2940)
 NEIKMLLEAGHVAVTSSGTGSMWACPNFSDGETHSSKISFTVEGPIAFFGLSNINGKH Hamster (frag 1)
 NEIKTLLEAGHVALTSSGTGSMWACPNFSDGETHSSQISFTVDGPIAFVGLSNINGKH Mouse (frag 1)
 LRWNQNLVYESGSLNFSKLEIQSQVDSQHWGHSVLTAQGMALFGEKGAEFTGRHDAHLNG Human (2941-3000)
 LRVIQKLAYESGFLNYSMLVEKSVESQHWGSSILTGKGTLLREAKAEMTGEHNAHLNG Hamster (frag 1)
 LRVIQKLTYESGFLNYSKFEVESQHWGSSILTANGRALLKDAKAEEMTGEHNAHLNG Mouse (frag 1)
 KVIIGTLKNSLFFSAQPFETASTNNEGNLKVRFPLRLTGKIDFLNNYALFLSPSAQAQSW Human (3001-3060)
 KVIIGTLKNSLFSQAQPFMITASTNDGNLKVSFPLKLTKGIDFLNNYALFLSPHAQAQSW Hamster (frag 1)
 KVIIGTLKNSLFFSAQPFETASTNNEGNLKVGFPKLTKGIDFLNNYALFLSPRAQAQSW Mouse (frag 1)

FIG. 14B1

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ALIGNMENT OF HUMAN 2701-3540 SEQ ID NO:214 WITH HAMSTER SEQ ID NO:215 AND MOUSE SEQ. ID NO:216 APOB-100 SEQUENCES

LNDQVPDLHIPEFQPLHSHTIEVPTFGKLYSILKIQSPLTLDANADIGNGTTSAEA-	Human (2701-2760)
EFQLPRLSHTIEIPAFGRLLHGLIKIQSPLTILDANANIQNWTTLENKAE	Hamster (frag 1)
EFQLPRLSHTIEIPAFGRLLHGLIKIQSPLTILDANANIQNWTTSGNKA	Mouse (frag 1)
GIAATITAKGESKLEVLNFDQANAQLSNPKINPLALKESVKFSKYLRTGEGSEMLFFG	Human (2761-2820)
IVASIAAT-GESEIALNFDQAAQFLELNPPLILKESMNFSSKHARMEHEGELFSG	Hamster (frag 1)
IVAS-VTAKGESQFEALNFDQAAQFLELNPHPVLKESMNFSSKHVRMEHEGEIVFDG	Mouse (frag 1)
NAIEGKSNTVASLHTEKNTLELSNGVIVKINNQLTLDSENTKYFHKLNTPKLDFFSSQADLR	Human (2821-2880)
KFIEGKLDTVASLQTEKNWVEFNMGMTVKINNPILDSHTKYFHKLSIPRLDFSSKASFN	Hamster (frag 1)
KATIEGKSDTVASLHTEKNEVEFNMGMTVKVNNQLTLDSTHTKYFHKLSVPRDLDFSSKASLN	Mouse (frag 1)
NEIKTLLKAGHTAWTSSGKGSWKACPRFSDEGTHESQISFTIEGPLTSFGLSNKINSKH	Human (2881-2940)
NEIKMLLEAGHVAMTSSGTGSNNMACPNFSDGTHSSKISFTVEGPIAFFGLSNNINGKH	Hamster (frag 1)
NEIKTLLEAGHVALTSSGTGSNNMACPNFSDGTHSSQISFTVDGPIAFVGLSNNINGKH	Mouse (frag 1)
LRVNNQLVYESGSLNFSKLEIQSQVDQSHVGHVLTAKGMALFEGGKAEFTGRHDAHLNG	Human (2941-3000)
LRVIQKLAYESGFLNYSMLVESKVESQHVGSILTGKGTVLRLREAKAEMTGEHNAHLNG	Hamster (frag 1)
LRVIQKLTYESGFLNYSKFEVESKVESQHVGSILTANGRALLKDKAEMTGEHNAHLNG	Mouse (frag 1)
KVIGTLKNSLFFSAQPFETASTNNEGILKVRFPRLTGKIDFLNNYALFLSPSAQAQSW	Human (3001-3060)
KVIGTLKNSLFFSAQPFMTASTNNDGILKVSPFLKLTGKIDFLNNYALFLSPHAQAQSW	Hamster (frag 1)
KVIGTLKNSLFFSAQPFETASTNNEGILKVGFPKLKLTGKIDFLNNYALFLSPRAQAQSW	Mouse (frag 1)

FIG. 14B2

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ALIGNMENT OF HUMAN 2701-3540 SEQ ID NO:214 WITH HAMSTER SEQ ID NO:215 AND MOUSE SEQ. ID
 NO:216 APOB-100 SEQUENCES

QVSARFNQYKYNQNSAGNNENIEAHVINGEANDLNLPTLTPEMRLPYTTITPPL	Human (3061-3120)
QVSARFNQYKYNQNSAGNNENIEAHVINGEANDLNLPTLTPEMRLPYTTITPPL	Hamster (frag 1)
QASTRFNQYKYNQNSAGNNENIEAHVINGEANDLNLPTLTPEMRLPYTTITPPL	Mouse (frag 1)
KDFSLEWETGLKEFLKTTKQSFDSLVAQYKKNKRRHSITNPLAVLCEFTSQSTKSFDRH	Human (3121-3180)
KDFSLEWETGLK-----KQSFDSLVAQYKKNRDRHSITATPLNGYEFILNNVDSGTGK	Hamster (frag 1)
KDFSLEWETGLKEFLKTTKQSFDSLVAQYKKNKSDKHSIVPLGMFYEFILNNVNSWDRK	Mouse (frag 1)
FEKRNNAALDFVTKSYNETKIKFDKYKAESQDELPRTFQIPGYTPVWVNEVSPFTTEM	Human (3181-3240)
TGKVRDSALDYLISSYNEAKNFEN-----SLIQPSRTFQKRGYTIIPFVNIETPFTVET	Hamster (frag 1)
FEKVRNNAALHFLTTSYNEAKTIKQYKNTENSINQPSGTQFNHGYTIPVWVNEVSPFAVET	Mouse (frag 1)
SAFGYVFPKAVSPFSILGSDVRVPSYTLILPSLELPVLHVPRNL-KLSLPHFKELCTIS	Human (3241-3300)
LASSHVIPKAINTPSVHILGNVIVPSYRLVLPSELPVLVRPNLLKFSLPDFKELRTID	Hamster (frag 1)
LASRHHVPTAISTPSVTIPGPNIMVPSYKLVLPPELPVFFHGPGLFKFFLPDFKGFNTID	Mouse (frag 1)
HIIFPAMGNITVDFSEKSSVITLNTNAELFNQSDIVAHLLSSSSSVTDALQYKLEGTIRL	Human (3301-3360)
NIYTPALGNFTVDFSEKSSVITLNTWGLYNRSDIVAHFLSSSSSVTDALQYKLEGTIRL	Hamster (frag 1)
NIYTPAMGNFTVDFSEKSSVITLNTWAGLYNQSDIVAHFLSSSSSVTDALQYKLEGTIRL	Mouse (frag 1)
TRKRGKLATALLSLNKFVESHNSTVSLTKKNMEVSVAKTTKAEI--PILRMNFQDELNGN	Human (3361-3420)
TRKRGKLATADSLTNKFKVGNHSDTSLTKKNMEASV-KTT-ANLHAPLITMNFQDELNGN	Hamster (frag 1)
MRKRGKLATAVSLTNKFKVGNHSDTSLTKKNMEASV-RTT-ANLHAPITMNFQDELNGN	Mouse (frag 1)

FIG. 14B3

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ALIGNMENT OF HUMAN 2701-3540 SEQ ID NO:214 WITH HAMSTER SEQ ID NO:215 AND MOUSE SEQ. ID
 NO:216 APOB-100 SEQUENCES

TKSKPTVSSMEFKYDFNSSMLYSTAKGAVDHKLSLESLSYFSIESSTKGDIKGSVLSR	Human (3421-3480)
AKSKPTIVSSSIELNYDFNSSKLYSTAKGGVDHKFSLESLSYFSIESSTKGNIKGSVLSQ	Hamster (frag 1)
TKSKPTVSSSIELNYDFNSSKLSHSTATGGIDHKFSLESLSYFSIESFTKGNIKSSFLSQ	Mouse (frag 1)
EYSGTIASEANTYLNKSTRSSVKLQGTSKIDDIWNLEVKENFAGEATLQRIYSLWEHST	Human (3481-3540)
EYSGSVASEANTYLNK	Hamster (frag 1)
EYSGSVANEANTYLNK	Mouse (frag 1)

FIG. 14B3 Cont.

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ALIGNMENT OF HUMAN 3481-4536 SEQ ID NO:217 WITH RAT SEQ ID NO:218 APOB-100 SEQUENCES

EYSGTIAEANTYLNKSKTRSSVYKLGTSKIDDIWNLEVKENFAGEATLQRIYSLWEHST	Human (3481-3540)
NSKGRSSVRLQGASNFAGIWNFEVGENFAGEATLRRIVGTWEHNM	Rat (frag 2)
KNHLQLEGLFFTINGEHTSKATLELSPWQMSALVQVHASQPSFFDFPDLGQEVANANTK	Human (3541-3600)
INHLQVFSYFDTKGQTCRATLELSPWTMTLLQVHVSQPSPLFDLHHFDQEVILKASTK	Rat (frag 2)
NQIRMKNEVRIHSGSFQSQVELSDQEKAHLDIAGSLEGLRFLKNTILPVYDKSLWDF	Human (3601-3660)
NQVSMKSEVQVESQVLQHNHFSNQDEEVRDLIAGSLEG-----QLWDL	Rat (frag 2)
-----	Human
ENFFLPAGKS-----	Rat (frag 2)
LKLDVTTSIGRRQHLRVSTAFVYTKNPNNGYSFIPVKVLADKFTIPGLKLNLDNSVLP	Human (3661-3720)
LR-ELLQIDGKQRYLQASTSLHYTKNPNGYLLSLPVQELTDRFIIPGLKLNDF-----	Rat (frag 2)
TFHVPTDLQVPSCKLDFREIQIYKKLRTSSFALNPTLPEVKFPEVDVLTKYSQPEDSL	Human (3721-3780)
-----SGIKIYKKLSTSPFALNLTMLPKVKFPGVDLLTQYSKPEGSS	Rat (frag 2)
IPFFEITVPESQLTVSRFTLPKSVSDGIAALDLNAVANKIADFELPTIIVPEQTEIIPSI	Human (3781-3840)
VPTFETIPEIQLTVSQFTLPKSPFVGNVTVDLTKLTLNLAQVDLPSITLPEQTEIIPSL	Rat (frag 2)
KFSVPAGIVIPSQALTARFEVDSPPVYNATWSASLKNKADYETVLDSTCSSTVQFLEYE	Human (3841-3900)
EFSVPAGIPIPFEGELTAHVGWASPLVYNTWSTGMKNKADHVEITFLDSTCSSTLQFLEYA	Rat (frag 2)

FIG. 14C1

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Alignment of Human 3481-4536 SEQ ID NO:217 with Rat SEQ ID NO:218 apob-100 Sequences	
LNLGTHKIEDGLASKTGTLAHRDFAEVEEDGKFEGLQEMEGKAHLNTKSPAFDTDLH	Human (3901-3960)
LKWGTHRIENDKFYIKTGTLQHCDFNVKYNEDGIFEGLDLGEAHLDTSPALTDHF	Rat (frag 2)
LRQDKKGKSTSAASPAVGTVMGMDDEDDDFSKWFFYSSPOSSPKKLTIFKTELVRRE	Human (3961-4020)
LHYKEDKTSVASAASPAIGTIVSLDASTDDQSRLHVFRPQSPDNKLSIFKMEWRDKE	Rat (frag 2)
SDEETQIKVNMEEEEAASGLLTSLKDNVPKATGVLYDVYVNYHMEHTGLTLREVSSKLRRN	Human (4021-4080)
SDGETYIKINWEEEAARLLDSLKSNVPKASEAVDYVKKYHLGH-----ASSELRKS	Rat (frag 2)
LQNAEWYQGAIRQIDIDVRFQKASGTTGTQOEWDKAQNLVQELLTOEGQASFOGL	Human (4081-4140)
LQNDAEH-----AIRMDEMNVAQRVTRDTYQSL-YKKMLAQE-----SQSIPEKL	Rat (frag 2)
KDNVFDGLVRVTQKFHMKVKHLIDSLIDFLNFPQFPQKPGIYTREELCTMFIREVGTV	Human (4141-4200)
KKMWLGSLLVRIITQKYHMAVTWLMDSVTHFLKFNRVQFPGNAGTYTVDELVTIAMRETKKL	Rat (frag 2)
LSQVYSKVHNGSEILFSYFQDLVTITLPFELRKHKLIDVITSMYRELLKDLKSEAQEVFKAI	Human (4201-4260)
LSQLF-----NGLGHLFSYVQDQV-----EKS RVINDI-----TFKCPFSP	Rat (frag 2)
QSLKTEVLRLNQDLLQFIFQLIEDNIKQLKEMKFTYLYNYTODEINTIFNDYIPYVFKL	Human (4261-4320)
TPCKLKVDLLIFREDNLNLGQQQDINFTTILSDFQSFLERLDIIIEEKIEC-LKNN--	Rat (frag 2)
-----	Human
ESTCVPDHIINMFFKTHIPFAFKS-----	Rat (frag 2)

FIG. 14C1 Cont.

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Alignment of Human 3481-4536 SEQ ID NO:217 with Rat SEQ ID NO:218 apoB-100
 Sequences

LKENLCLNHLKFNELIQELQEQASQELQOIHQYIMALREEYFDPISIVGWTVKYYELEEKI	Human (4321-4380)
LRENIYSVFSEFNDVQSILQEGSYKIQVHQYMKAFREEYFDPISVWGTVKYYEIEEKM	Rat (frag 2)
VSLIKNLLVALKDFHSEYIVSASNFTSQLSSQVEQFLHRNIQEYLSILTDPGKGKEKIA	Human (4381-4440)
VDLIKTLAPLRDFYSEYSVTAADFASKMSTQVEQFVSROIREFYLSMLADINGKGREKVA	Rat (frag 2)
ELSATAQEIISKQAIATKKIISDYHQQFRYKLQDFSDQLSDYVEKFAIESKRLIDLSIQN	Human (4441-4500)
ELSIVVKERIKSWSTAVAEITS DYLRQLHSKLQDFSDQLSGYVEKFAESTRLIDLSIQN	Rat (frag 2)
YHTFLIYITELLKKLQSTTVMN--PYMKLAPGELTIIL	Human (4501-4536)
YHMFRLYIAELLKKLQVATANNVSPYLRFAQGELIITF	Rat (frag 2)

FIG. 14C2

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Alignment of Human 4141-4536 SEQ ID NO:219 with Chicken SEQ ID NO:220 apoB-100 Sequences

KDWFDGLVRVYQKFHMVKYKHLIDSLIDFLNPRFQPGKPGIVTREELCTMFIREVGTV	Human (4141-4200)
IPGLSEKYTGEELYLMTTEKAAKT	Chicken (frag 1)
LSQVSKVHNGSEILFSYFQDLVITLPELKKHLIDVISMYRELLKDLSCAEQEVFKAI	Human (4201-4260)
ADICLSKLQEVFDALIAATSELEVRVPASSETILRGRNVLDOIKENLKHLEKIRQTFVTL	Chicken (frag 1)
QSLKTTEVLRLQDLLQTFIQLIEDNIKQLKEMKFTYLINVIQDEINTIFNDYIPYVFKL	Human (4261-4320)
QEADFAGKLRKQVWQKTFQKAGNMVRSLSKKNFEDIKVQMQLYKQAMASDYAHKLR	Chicken (frag 1)
LKENCLNLHKFNEFIQNELQEASQELQIQHYIMALREYFDPDSIVGTVKYVELEEKI	Human (4321-4380)
LAENWKYISQIKNFSQKTLQKLSNLQQLVLYIKALREYFDPDTLGMVSVYVEDEKV	Chicken (frag 1)
VSLIKNLLVALKDFHSEYIVSASNFTSOLSSQVEQFLHRNIQEYLSILTDPPGKGKEKIA	Human (4381-4440)
LGLLKNLMDTLVIWYNEVAKDLSLVTRLTDQVRELVENYRQEYDYDLITDVEGKGRQKVM	Chicken (frag 1)
ELSATAQEIIKSQAATKKIISDYHQQFRYKQLQDFSDQLSDYVEKFAESKRLIDLSIQN	Human (4441-4500)
ELSSAAQEKIRYWSAVAKRKINEHNRQVKAQLQEIYGQLSDSQEKLINNAKMLIDLTV EK	Chicken (frag 1)
YHTFLIYITELLKKLQSTTMNPMKLAGELTIIL-----	Human (4501-4536)
YSTFMKYIFELLRWFEQATADSTIKPYIAVREGELRIDVPFDWEYINQMPOKSRREALRNKV	Chicken (frag 1)
-----	Human
ELTRALIQQGVQGTGRKMEEMQAFIDEQLATEQLSFQQIIVENIQKRMKT	Chicken (frag 1)

FIG. 14D

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Alignment of Human 1561-1740 SEQ ID NO:221 with Rabbit SEQ ID NO:222 apoB-100
 Sequences

DMTFKQNALLRSEYQADYESLRFFSLLSGSLNSHGLELNADILGTDKINS GA HKATLRI	Human (1561-1620)
DLTFKQNALLRSEYQADYKSLRFFTL SG LLNTHGLELNADILGTDK MT AAHKATLRI	Rabbit (frag 1)
GQDGI ST SATTNLKCSLLVLENELNAELGLSGASMKLT TNG RFREHNAKFS LDG KAALTE	Human (1621-1680)
GQNGV ST SATTSLRYSPPLMLENELNAELALSGASMKLATNGRFKEHNAKFS LDG KATLTE	Rabbit (frag 1)
LSLGSAYQAMILGVDSKNIFNFKVY Q EGLKLSNDMMGSYAEMKFDHTNSLNIAGLSLDFS	Human (1681-1740)
LSLGSAYQAMILGADSKNIFNF-----	Rabbit (frag 1)

FIG. 14E

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Alignment of Human 3301-3720 SEQ ID NO:223 with Rabbit SEQ ID NO:224 apoB-100 Sequences	
<u>H</u> I <u>F</u> I <u>P</u> A <u>G</u> N <u>I</u> T <u>Y</u> D <u>F</u> S <u>K</u> S <u>I</u> T <u>L</u> N <u>T</u> N <u>A</u> E <u>L</u> F <u>N</u> G <u>S</u> D <u>I</u> V <u>A</u> H <u>L</u> L <u>S</u> S <u>S</u> S <u>I</u> D <u>A</u> L <u>Q</u> <u>K</u> L <u>E</u> G <u>T</u> T <u>R</u> L - M <u>A</u> S <u>E</u> K <u>G</u> P <u>S</u> N <u>K</u> D <u>Y</u> T	Human (3301-3360) Rabbit (frag 2)
T <u>R</u> K <u>R</u> G <u>L</u> K <u>L</u> A <u>T</u> A <u>L</u> S <u>L</u> S <u>N</u> K <u>F</u> V <u>E</u> G <u>S</u> H <u>N</u> S <u>T</u> V <u>S</u> L <u>T</u> T <u>K</u> N <u>M</u> E <u>V</u> S <u>V</u> A <u>K</u> T <u>T</u> K <u>A</u> E <u>I</u> P <u>I</u> L <u>R</u> M <u>N</u> F <u>K</u> Q <u>E</u> L <u>N</u> G <u>N</u> L <u>R</u> R <u>R</u> I - - - - - E <u>P</u> N <u>E</u> F <u>E</u> V <u>F</u> D <u>P</u> Q <u>E</u> L <u>R</u> K <u>E</u> A <u>C</u> L <u>L</u> Y <u>E</u> T <u>K</u> W <u>G</u> A <u>S</u> S <u>K</u> T <u>W</u> R <u>S</u> G <u>K</u> N <u>T</u> T <u>N</u> H - V <u>E</u> V <u>N</u> - - - - -	Human (3361-3420) Rabbit (frag 2)
F <u>L</u> E <u>K</u> L <u>T</u>	Human
T <u>K</u> S <u>K</u> P <u>T</u> V <u>S</u> S <u>S</u> M <u>E</u> F <u>K</u> Y <u>D</u> F <u>N</u> S <u>S</u> M <u>L</u> Y <u>S</u> T <u>A</u> G <u>A</u> V <u>H</u> K <u>L</u> S <u>L</u> E <u>S</u> L <u>T</u> S <u>F</u> S <u>T</u> E <u>S</u> T <u>K</u> G <u>D</u> V <u>K</u> G <u>S</u> V <u>L</u> S <u>R</u> - - - - -	Rabbit (frag 2)
E <u>Y</u> S <u>G</u> T <u>I</u> A <u>S</u> E <u>A</u> N <u>T</u> Y <u>L</u> N <u>S</u> K <u>S</u> T <u>R</u> S <u>S</u> V <u>K</u> L <u>O</u> G <u>T</u> S <u>K</u> I <u>D</u> D <u>I</u> W <u>L</u> E <u>V</u> K <u>E</u> N <u>F</u> A <u>G</u> E <u>A</u> T <u>L</u> Q <u>R</u> I <u>Y</u> S <u>L</u> W <u>E</u> H <u>S</u> T R <u>K</u> E <u>A</u> C <u>L</u> L <u>Y</u> E <u>T</u> K <u>W</u> G <u>A</u> S <u>S</u> K <u>T</u> W <u>R</u> S <u>G</u> K - N <u>T</u> T <u>N</u> H <u>V</u> E <u>N</u> F - L <u>E</u> - K <u>L</u> T <u>S</u> E <u>G</u> R <u>L</u> G <u>P</u> S <u>T</u> C <u>C</u> S <u>I</u> - - - - -	Human (3421-3480) Rabbit (frag 2)
K <u>N</u> H <u>L</u> Q <u>L</u> E <u>G</u> L <u>F</u> F <u>T</u> N <u>G</u> E <u>H</u> T <u>S</u> K <u>A</u> T <u>L</u> E <u>S</u> P <u>W</u> M <u>S</u> A <u>L</u> V <u>Q</u> V <u>H</u> A <u>S</u> Q <u>P</u> S <u>S</u> F <u>H</u> D <u>P</u> D <u>L</u> G <u>Q</u> E <u>V</u> A <u>L</u> N <u>A</u> N <u>T</u> K T <u>W</u> F <u>L</u> S <u>W</u> S - - P <u>W</u> E <u>C</u> S <u>M</u> A <u>I</u> R <u>E</u> F <u>L</u> S <u>Q</u> H <u>P</u> G <u>V</u> T <u>L</u> I <u>I</u> F <u>V</u> A <u>R</u> L <u>F</u> Q <u>H</u> M <u>D</u> R <u>R</u> N <u>R</u> Q <u>G</u> L <u>K</u> D <u>L</u> V <u>T</u> S <u>G</u> V <u>T</u> W <u>R</u> N <u>O</u> K <u>I</u> R <u>W</u> K <u>N</u> E <u>V</u> R <u>I</u> H <u>S</u> S <u>F</u> Q <u>S</u> O <u>V</u> E <u>L</u> S <u>N</u> D <u>Q</u> E <u>K</u> A <u>H</u> D <u>I</u> A <u>G</u> S <u>L</u> E <u>G</u> H <u>L</u> R <u>E</u> L <u>K</u> N <u>I</u> L <u>P</u> V <u>Y</u> D <u>K</u> S <u>L</u> W <u>D</u> F V <u>N</u> S <u>V</u> E <u>Y</u> C <u>Y</u> C <u>W</u> E <u>N</u> F <u>V</u> N <u>Y</u> P <u>P</u> G <u>K</u> A <u>Q</u> W <u>P</u> R <u>I</u> P <u>P</u> R <u>M</u> L <u>M</u> Y <u>A</u> L <u>E</u> Y <u>I</u> C <u>I</u> L <u>G</u> L <u>P</u> P <u>C</u> - - - - -	Human (3481-3540) Rabbit (frag 2)
L <u>K</u> D <u>V</u> T <u>T</u> S <u>I</u> G <u>R</u> R <u>Q</u> H <u>L</u> R <u>V</u> S <u>T</u> A <u>F</u> V <u>T</u> K <u>N</u> P <u>N</u> G <u>Y</u> S <u>F</u> S <u>I</u> P <u>K</u> V <u>K</u> L <u>A</u> D <u>K</u> F <u>I</u> T <u>P</u> G <u>L</u> K <u>N</u> D <u>L</u> N <u>S</u> V <u>L</u> W <u>P</u> - - - - - L <u>K</u> I <u>S</u> R <u>R</u> H <u>Q</u> K <u>Q</u> L - - - - - T <u>F</u> F <u>S</u> L <u>T</u> P <u>Q</u> Y <u>C</u> H <u>Y</u> K <u>M</u> I <u>P</u> P <u>Y</u> I <u>L</u> L <u>A</u> T <u>G</u> L <u>L</u> Q <u>P</u> S <u>V</u> P <u>W</u> R	Human (3541-3600) Rabbit (frag 2)
	Human (3601-3660) Rabbit (frag 2)
	Human (3661-3720) Rabbit (frag 2)

FIG. 14F

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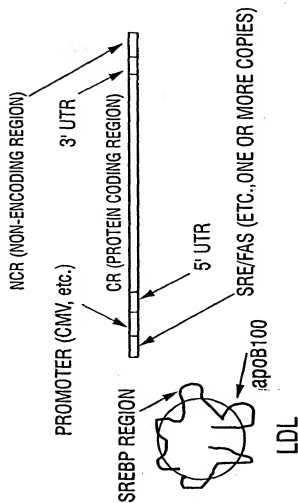


FIG. 15